OM of: US-09-784-340-2 to: N_Geneseq_0601:* out_format : pfs

Date: Aug 27, 2001 8:14 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09784340/runat_27082001_123147_132/app_query.fasta_1.591
-DB=N_Geneseq_0601 -QFMT=fastap -SUFFIX=olip2n.rng -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=US09784340_@CGN1_1_236 -NCPU=6 -ICPU=3
-LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-784-340-2
Query length: 527
Database: N_Geneseq_0601:*
Database sequences: 730101
Database length: 313950809
Search time (sec): 112.140000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	!	Documentation	..
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC65396	+	174.00	3215.51	3.9e-171	1650	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV87412	+	157.00	2907.02	6.0e-154	515	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC03286	+	116.00	2144.69	1.7e-111	350	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95198	+	33.00	584.09	1.5e-24	1589	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95199	+	33.00	582.02	1.9e-24	2092	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV15900	+	33.00	581.96	1.9e-24	2107	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95205	+	28.00	498.18	8.9e-20	596	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95200	+	28.00	489.61	2.7e-19	1854	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95211	+	23.00	401.12	2.3e-14	978	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95206	+	23.00	395.80	4.5e-14	1976	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95210	+	15.00	248.07	7.6e-06	1602	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95197	+	13.00	217.12	0.0004	689	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95209	+	12.00	201.19	0.0031	480	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95194	+	12.00	197.85	0.0047	746	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95208	+	12.00	195.49	0.0064	1020	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95203	+	12.00	191.10	0.0113	1822	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95202	+	11.00	174.76	0.0917	1340	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA87255	+	10.00	169.65	0.1767	223	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA87473	+	10.00	168.52	0.2043	259	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA87085	+	10.00	165.91	0.2856	366	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95204	+	10.00	154.80	1.19	1591	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA87154	+	9.00	153.31	1.44	164	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ07208	+	9.00	146.74	3.34	391	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC79066	+	9.00	146.74	3.34	391	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC98478	+	9.00	144.77	4.30	508	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ33025	+	9.00	144.02	4.73	561	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ45118	+	9.00	141.97	6.15	735	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95196	+	9.00	138.67	9.40	1138	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC45295	+	9.00	136.88	11.82	1442	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC39489	+	9.00	136.87	11.84	1444	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ33027	+	9.00	135.78	13.61	1667	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95207	+	9.00	133.31	18.68	2312	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ27369	+	9.00	133.18	18.99	2351	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ27370	+	9.00	133.13	19.12	2368	!		
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/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95057	+	8.00	148.28	2.74	27	!	H	
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95058	+	8.00	148.28	2.74	27	!	H	
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ99349	-	8.00	139.27	8.70	89	!	H	
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAF15707	+	8.00	131.05	24.97	264	!		
/SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV87432	+	8.00	129.32	31.19	332			
/SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ60202	+	8.00	127.50	39.35	422			
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ99332	+	8.00	127.29	40.44	434			
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ99331	+	8.00	127.24	40.71	437			
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ99330	+	8.00	127.14	41.25	443			
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ99338	+	8.00	126.40	45.31	488			

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC65396

seq_documentation_block:
ID AAC65396 standard; cDNA; 1650 BP.
XX
AC AAC65396;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human carbohydrate-modifying enzyme cDNA Incyte ID No: 2912330CB1.
XX
KW Human; carbohydrate-modifying enzyme; CME; antidiabetic;
KW immunosuppressive; anti-HIV; antiinflammatory; antianaemic;
KW antiasthmatic; antiarteriosclerotic; antithyroid; hepatotropic;
KW nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic;
KW antiarthritic; antipsoriatic; uropathic; ophthalmological;
KW dermatological; antiulcer; cytostatic; virucide; antibacterial;
KW fungicide; protozoacide; tranquiliser; vulnerary; diabetes;
KW autoimmune disorder; inflammatory disorder; infection; ss.
XX
OS Homo sapiens.
XX
PN WO200063351-A2.
XX
PD 26-OCT-2000.
XX
PF 20-APR-2000; 2000WO-US10882.
XX
PR 21-APR-1999; 99US-0130383.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, Tang YT, Hillman JL, Baughn MR, Yang J;
XX
DR WPI; 2000-672729/65.
DR P-PSDB; AAB28677.
XX
PT Novel carbohydrate modifying enzyme polypeptides and polynucleotides
PT for diagnosis, treatment, and prevention of carbohydrate metabolism
PT disorders, autoimmune/inflammatory disorders, and cancer -
XX
PS Claim 4; Page 75; 75pp; English.
XX
CC The present cDNA sequence encodes a human carbohydrate-modifying enzyme
CC (CME). CME polynucleotides and polypeptides are useful for treating and
CC diagnosing diseases associated with CME such as diabetes,
CC autoimmune/inflammatory disorders such as AIDS, Addison's disease,
CC adult respiratory distress syndrome, allergies, anaemia, asthma,
CC atherosclerosis, autoimmune thyroiditis, bronchitis, cholocystitis,
CC contact dermatitis, Crohn's disease, emphysema, erythroblastosis fetalis,
CC glomerulonephritis, Good pasture's syndrome, gout, Grave's disease,
CC Hashimoto's thyroiditis, multiple sclerosis, myasthenia gravis,
CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC Reiter's syndrome, arthritis, scleroderma, sjogren's syndrome, systemic
CC lupus erythematosus, ulcerative colitis, uveitis, Werner syndrome,
CC complications of cancer, haemodialysis, and extracorporeal circulation,
CC viral, bacterial, fungal parasitic, protozoal, and helminthic infections,
CC trauma, or cancer. CME, or its catalytic or immunogenic fragment, is
CC useful for drug screening.
XX
SQ Sequence 1650 BP; 489 A; 330 C; 354 G; 477 T; 0 other;

alignment_scores:
Quality: 174.00 Length: 174
Ratio: 1.000 Gaps: 0

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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAC65396   ..

 Align seg 1/1  to: AAC65396  from: 1  to: 1650

     354 TrpIleProGlnAsnAspLeuLeuGlyHisProLysThrLysAlaPheIl 370
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1100 TGGATACCCCAGAATGATCTTCTTGGTCATCCCAAAACCAAAGCTTTTAT 1149

     370 eThrHisGlyGlyMetAsnGlyIleTyrGluAlaIleTyrHisGlyValP 387
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1150 CACTCATGGTGGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCC 1199

     387 roMetValGlyValProIlePheGlyAspGlnLeuAspAsnIleAlaHis 403
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1200 CTATGGTGGGAGTTCCCATATTTGGTGATCAGCTTGATAACATAGCTCAC 1249

     404 MetLysAlaLysGlyAlaAlaValGluIleAsnPheLysThrMetThrSe 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1250 ATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAACTATGACAAG 1299

     420 rGluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrL 437
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1300 CGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCCTCTTATA 1349

     437 ysGluAsnAlaMetArgLeuSerArgIleHisHisAspGlnProValLys 453
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1350 AAGAGAATGCTATGAGATTATCAAGAATTCACCATGATCAACCTGTAAAG 1399

     454 ProLeuAspArgAlaValPheTrpIleGluPheValMetArgHisLysGl 470
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1400 CCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCATGCGCCACAAAGG 1449

     470 yAlaLysHisLeuArgSerAlaAlaHisAspLeuThrTrpPheGlnHisT 487
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1450 AGCCAAGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCCAGCACT 1499

     487 yrSerIleAspValIleGlyPheLeuLeuThrCysValAlaThrAlaIle 503
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1500 ACTCTATAGATGTGATTGGGTTCCTGCTGACCTGTGTGGCAACTGCTATA 1549

     504 PheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysTh 520
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1550 TTCTTGTTCACAAAATGTTTTTTATTTTCCTGTCAAAAATTTAATAAAAC 1599

     520 rArgLysIleGluLysArgGlu 527
         ||||||||||||||||||||||
    1600 TAGAAAGATAGAAAAGAGGGAA 1621

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV87412

seq_documentation_block:
ID   AAV87412 standard; cDNA; 515 BP.
XX
AC   AAV87412;
XX
DT   27-APR-1999  (first entry)
XX
DE   EST clone BR77.
XX
KW   Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW   tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW   chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW   receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
OS   Homo sapiens.
XX
PN   WO9845435-A2.
XX
PD   15-OCT-1998.
XX
PF   10-APR-1998;   98WO-US06954.
XX
PR   10-APR-1997;   97US-0835913.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ,  Jacobs K,  Lavallie ER,  McCoy JM,  Merberg D;
PI   Racie LA,  Spaulding V,  Treacy M;
XX
DR   WPI; 1999-070076/06.
XX
PT   New polynucleotides encoding human secreted proteins - derived from
PT   e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT   ovary, pituitary, retina and colon cDNA libraries
XX
PS   Claim 1; Page 556; 633pp; English.
XX
CC   This sequence represents an expressed sequence tag (EST), and is a
CC   polynucleotide of the invention. The polynucleotides of the invention are
CC   all secreted EST sequences isolated from a variety of human tissue
CC   sources. The EST sequences and proteins encoded by them are predicted to
CC   have useful biological activities which would make them suitable for
CC   treating, preventing or ameliorating medical conditions in humans and
CC   animals, although no supporting data is given. Suggested activities
CC   include nutritional activity, immune stimulating or suppressing activity,
CC   haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC   activity. The EST sequences are also stated to be useful for gene
CC   therapy.
XX
SQ   Sequence 515 BP; 148 A; 98 C; 122 G; 147 T; 0 other;

alignment_scores:
           Quality:  157.00              Length:    157
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAV87412   ..

 Align seg 1/1  to: AAV87412  from: 1  to: 515

       1 MetArgSerAspLysSerAlaLeuValPheLeuLeuLeuGlnLeuPheCy 17
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      33 ATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCTG 82

      17 sValGlyCysGlyPheCysGlyLysValLeuValTrpProCysAspMetS 34
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      83 TGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGA 132

      34 erHisTrpLeuAsnValLysValIleLeuGluGluLeuIleValArgGly 50
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     133 GCCATTGGCTTAATGTCAAGGTCATTCTAGAAGAGCTCATAGTGAGAGGC 182

      51 HisGluValThrValLeuThrHisSerLysProSerLeuIleAspTyrAr 67
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     183 CATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACAG 232

      67 gLysProSerAlaLeuLysPheGluValValHisMetProGlnAspArgT 84
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     233 GAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAA 282

      84 hrGluGluAsnGluIlePheValAspLeuAlaLeuAsnValLeuProGly 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     283 CAGAAGAAAATGAAATATTTGTTGACCTAGCTCTGAATGTCTTGCCAGGC 332

     101 LeuSerThrTrpGlnSerValIleLysLeuAsnAspPhePheValGluIl 117
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     333 TTATCAACCTGGCAATCAGTTATAAAATTAAATGATTTTTTTGTTGAAAT 382
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     117 eArgGlyThrLeuLysMetMetCysGluSerPheIleTyrAsnGlnThrL 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     383 AAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGC 432

     134 euMetLysLysLeuGlnGluThrAsnTyrAspValMetLeuIleAspPro 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     433 TTATGAAGAAGCTACAGGAAACCAACTACGATGTAATGCTTATAGACCCT 482

     151 ValIleProCysGlyAspLeu 157
         |||||||||||||||||||||
     483 GTGATTCCCTGTGGAGACCTG 503

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC03286

seq_documentation_block:
ID   AAC03286 standard; cDNA; 350 BP.
XX
AC   AAC03286;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 3284.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   P-PSDB; AAG03280.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures
XX
PS   Claim 1; SEQ ID 3284; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. An ORF has been identified within the
CC   sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC   derived from 30 different tissues. EST sequences usually correspond
CC   mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC   often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC   well suited for isolating cDNA sequences derived from the 5' ends of
CC   mRNAs and even in those cases where longer cDNA sequences have been
CC   obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC   mRNAs with intact 5' ends and can therefore be used to obtain full length
CC   cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC   gene therapy and chromosome mapping procedures. They are used to obtain
CC   upstream regulatory sequences and to design expression and secretion
CC   vectors.
XX
SQ   Sequence 350 BP; 108 A; 69 C; 77 G; 96 T; 0 other;


alignment_scores:
           Quality:  116.00            Length:    116
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:

US-09-784-340-2 x AAC03286   ..

Align seg 1/1  to: AAC03286  from: 1  to: 350

     252 GluIleTrpLeuIleArgThrTyrTrpAspPheGluPheProGlnProTy 268
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCCTCAACCATA 50

     268 rGlnProAsnPheGluPheValGlyGlyLeuHisCysLysProAlaLysA 285
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 CCAACCTAACTTTGAGTTTGTTGGAGGATTGCACTGTAAACCTGCCAAAG 100

     285 laLeuProLysGluMetGluAsnPheValGlnSerSerGlyGluAspGly 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 CTTTGCCTAAGGAAATGGAAAATTTTGTCCAGAGTTCAGGGGAAGATGGT 150

     302 IleValValPheSerLeuGlySerLeuPheGlnAsnValThrGluGluLy 318
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 ATTGTGGTGTTTTCTCTGGGGTCACTGTTTCAAAATGTTACAGAAGAAAA 200

     318 sAlaAsnIleIleAlaSerAlaLeuAlaGlnIleProGlnLysValLeuT 335
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 GGCTAATATCATTGCTTCAGCCCTTGCCCAGATCCCACAGAAGGTGTTAT 250

     335 rpArgTyrLysGlyLysLysProSerThrLeuGlyAlaAsnThrArgLeu 351
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 GGAGGTACAAAGGAAAAAAACCATCCACATTAGGAGCCAATACTCGGCTG 300

     352 TyrAspTrpIleProGlnAsnAspLeuLeuGlyHisProLysThrLys 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TATGATTGGATACCCCAGAATGATCTTCTTGGTCATCCCAAAACCAAA 348

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95198

seq_documentation_block:
ID   AAZ95198 standard; DNA; 1589 BP.
XX
AC   AAZ95198;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B4 exon 6 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B4; UGT2B4; polymorphism; metabolism; SNPs;
KW   drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions
XX
PS   Example 1; Page 33-34; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 6 of the human
CC   UDP-glucuronosyltransferase 2B4 (UGT2B4) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC   the glucuronic acid conjugation of a wide range of endogenous and
CC   exogenous substrates. The UGT2B gene subfamily encode steroid
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CC   metabolizing isoforms in the liver. Alteration of the expression or
CC   function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC   can be used to detect altered UGT2B metabolism of a substrate in an
CC   individual. The nucleic acid molecules comprising a human UGT2B sequence
CC   polymorphism can be used in screening assays for genotyping individuals,
CC   also to predict their rate of metabolism of UGT2B substrate, potential
CC   drug-drug interactions and adverse side effects. The polymorphisms can be
CC   used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC   linkage related to phenotypic variation in activity or expression of
CC   UGT2B protein. The polymorphism containing nucleic acid molecules may
CC   also be used for generating genetically modified non-human animals and
CC   for obtaining site specific gene modification in cell lines.
XX
SQ   Sequence 1589 BP; 467 A; 312 C; 293 G; 517 T; 0 other;


alignment_scores:
            Quality:   33.00              Length:     33
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95198    ..

 Align seg 1/1  to: AAZ95198  from: 1  to: 1589

     443 LeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaVa 459
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     753 TTATCAAGAATTCATCATGATCAACCAGTGAAGCCCCTTGATCGAGCAGT 802

     459 lPheTrpIleGluPheValMetArgHisLysGlyAlaLysHisLeuArg 475
         |||||||||||||||||||||||||||||||||||||||||||||||||
     803 CTTCTGGATTGAATTTGTCATGCGCCATAAAGGAGCCAAGCACCTTCGG 851

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95199

seq_documentation_block:
ID   AAZ95199 standard; DNA; 2092 BP.
XX
AC   AAZ95199;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UDP-glucuronosyltransferase 2B4 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B4; UGT2B4; polymorphism; metabolism; SNPs;
KW   drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
DR   P-PSDB; AAY78933.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions -
XX
PS   Disclosure; Page 34-36; 72pp; English.
XX
```

```
CC   This sequence represents the human UDP-glucuronosyltransferase 2B4
CC   (UGT2B4) gene. UDP-glucuronosyltransferase (UGTs) are a family of
CC   enzymes that catalyse the glucuronic acid conjugation of a wide range of
CC   endogenous and exogenous substrates. The UGT2B gene subfamily encode
CC   steroid metabolizing isoforms in the liver. Alteration of the expression
CC   or function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms (see AAZ95051-Z95110). Probes which detect the
CC   UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism
CC   of a substrate in an individual. The nucleic acid molecules comprising a
CC   human UGT2B sequence polymorphism can be used in screening assays for
CC   genotyping individuals, also to predict their rate of metabolism of
CC   UGT2B substrate, potential drug-drug interactions and adverse side
CC   effects. The polymorphisms can be used as single nucleotide polymorphisms
CC   (SNPs) for detecting genetic linkage related to phenotypic variation in
CC   activity or expression of UGT2B protein. The polymorphism containing
CC   nucleic acid molecules may also be used for generating genetically
CC   modified non-human animals and for obtaining site specific gene
CC   modification in cell lines.
XX
SQ   Sequence 2092 BP; 639 A; 398 C; 438 G; 617 T; 0 other;


alignment_scores:
            Quality:   33.00              Length:     33
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95199    ..

 Align seg 1/1  to: AAZ95199  from: 1  to: 2092

     443 LeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaVa 459
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1370 TTATCAAGAATTCATCATGATCAACCAGTGAAGCCCCTTGATCGAGCAGT 1419

     459 lPheTrpIleGluPheValMetArgHisLysGlyAlaLysHisLeuArg 475
         |||||||||||||||||||||||||||||||||||||||||||||||||
    1420 CTTCTGGATTGAATTTGTCATGCGCCATAAAGGAGCCAAGCACCTTCGG 1468

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV15900

seq_documentation_block:
ID   AAV15900 standard; cDNA; 2107 BP.
XX
AC   AAV15900;
XX
DT   26-MAY-1998  (first entry)
XX
DE   Uridine diphospho-glucuronosyltransferase 2B17 (UGT2B17) encoding cDNA.
XX
KW   Uridine diphospho-glucuronosyltransferase 2B17; UGT2B17; catalyse;
KW   androsterone; androsterone-glucuronic acid; androgen; enzyme; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..51
FT                   /*tag=  a
FT   CDS             52..1644
FT                   /*tag=  b
FT                   /product= "UGTB17 enzyme"
FT   3'UTR           1645..2107
FT                   /*tag=  c
XX
PN   WO9744466-A1.
XX
PD   27-NOV-1997.
XX
PF   16-MAY-1997;   97WO-CA00328.
XX
PR   17-MAY-1996;   96US-0649319.
```

```
XX
PA   (ENDO-) ENDORECHERCHE INC.
XX
PI   Beaulieu M,  Belanger A,  Hum DW,  Levesque E;
XX
DR   WPI; 1998-018520/02.
DR   P-PSDB; AAW47126.
XX
PT   DNA encoding uridine di:phospho:glucuronosyl:transferase 2B17 -
PT   which catalyses conversion of androsterone to
PT   androsterone-glucuronic acid
XX
PS   Claim 15; Pages 4-6; 53pp; English.
XX
CC   This cDNA encodes an enzyme uridine di-phosphoglucuronosyltransferase
CC   2B17 (UGT2B17). This novel enzyme catalyses the conversion of
CC   androsterone to androsterone-glucuronic acid. The UGT2B17 can be used to
CC   detect anti-UGT2B17 antibodies. The antibody can be used to detect a
CC   localised concentration of UGT2B17 or an alteration in androgen activity.
CC   The UGT2B17 can also be used to alter the concentration of an androgenic
CC   compound in a tissue, specifically dihydrotestosterone. An isolated
CC   nucleotide sequence comprising at least 30 consecutive nucleotides from
CC   the coding region of the 2107 base pair sequence, or its complement can
CC   be used to block the synthesis of UGT2B17, e.g. an expression disrupting
CC   sense or antisense fragment, or as a probe for a UGT2B17 coding sequence.
XX
SQ   Sequence 2107 BP; 657 A; 382 C; 424 G; 644 T; 0 other;


alignment_scores:
            Quality:   33.00              Length:     33
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAV15900   ..

 Align seg 1/1  to: AAV15900  from: 1  to: 2107

     443 LeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaVa 459
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1387 TTATCAAGAATTCATCATGATCAACCGGTGAAGCCCCTGGATCGAGCAGT 1436

     459 lPheTrpIleGluPheValMetArgHisLysGlyAlaLysHisLeuArg 475
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1437 CTTCTGGATTGAGTTTGTCATGCGCCATAAAGGAGCCAAGCACCTTCGG 1485

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95205

seq_documentation_block:
ID   AAZ95205 standard; DNA; 596 BP.
XX
AC   AAZ95205;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B7 exon 5 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B7; UGT2B7; polymorphism; metabolism; SNPs;
KW   drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions
XX
PS   Example 2; Page 47-48; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 5 of the human
CC   UDP-glucuronosyltransferase 2B7 (UGT2B7) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC   the glucuronic acid conjugation of a wide range of endogenous and
CC   exogenous substrates. The UGT2B gene subfamily encode steroid
CC   metabolizing isoforms in the liver. Alteration of the expression or
CC   function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC   can be used to detect altered UGT2B metabolism of a substrate in an
CC   individual. The nucleic acid molecules comprising a human UGT2B sequence
CC   polymorphism can be used in screening assays for genotyping individuals,
CC   also to predict their rate of metabolism of UGT2B substrate, potential
CC   drug-drug interactions and adverse side effects. The polymorphisms can be
CC   used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC   linkage related to phenotypic variation in activity or expression of
CC   UGT2B protein. The polymorphism containing nucleic acid molecules may
CC   also be used for generating genetically modified non-human animals and
CC   for obtaining site specific gene modification in cell lines.
XX
SQ   Sequence 596 BP; 199 A; 97 C; 115 G; 185 T; 0 other;


alignment_scores:
            Quality:   28.00              Length:     28
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95205   ..

 Align seg 1/1  to: AAZ95205  from: 1  to: 596

     448 HisAspGlnProValLysProLeuAspArgAlaValPheTrpIleGluPh 464
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 CATGATCAACCAGTGAAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATT 106

     464 eValMetArgHisLysGlyAlaLysHisLeuArg 475
         |||||||||||||||||||||||||||||||||
     107 TGTCATGCGCCACAAAGGAGCTAAACACCTTCGG 140

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95200

seq_documentation_block:
ID   AAZ95200 standard; DNA; 1854 BP.
XX
AC   AAZ95200;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UDP-glucuronosyltransferase 2B7 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B7; UGT2B7; polymorphism; metabolism; SNPs;
KW   drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
```

```
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
DR   P-PSDB; AAY78934.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions -
XX
PS   Disclosure; Page 41-44; 72pp; English.
XX
CC   This sequence represents the human UDP-glucuronosyltransferase 2B7
CC   (UGT2B7) gene. UDP-glucuronosyltransferase (UGTs) are a family of
CC   enzymes that catalyse the glucuronic acid conjugation of a wide range of
CC   endogenous and exogenous substrates. The UGT2B gene subfamily encode
CC   steroid metabolizing isoforms in the liver. Alteration of the expression
CC   or function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms (see AAZ95051-Z95110). Probes which detect the
CC   UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism
CC   of a substrate in an individual. The nucleic acid molecules comprising a
CC   human UGT2B sequence polymorphism can be used in screening assays for
CC   genotyping individuals, also to predict their rate of metabolism of
CC   UGT2B substrate, potential drug-drug interactions and adverse side
CC   effects. The polymorphisms can be used as single nucleotide polymorphisms
CC   (SNPs) for detecting genetic linkage related to phenotypic variation in
CC   activity or expression of UGT2B protein. The polymorphism containing
CC   nucleic acid molecules may also be used for generating genetically
CC   modified non-human animals and for obtaining site specific gene
CC   modification in cell lines.
XX
SQ   Sequence 1854 BP; 572 A; 338 C; 392 G; 552 T; 0 other;


alignment_scores:
            Quality:   28.00              Length:     28
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95200   ..

 Align seg 1/1  to: AAZ95200  from: 1  to: 1854

     448 HisAspGlnProValLysProLeuAspArgAlaValPheTrpIleGluPh 464
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1362 CATGATCAACCAGTGAAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATT 1411

     464 eValMetArgHisLysGlyAlaLysHisLeuArg 475
         |||||||||||||||||||||||||||||||||||
    1412 TGTCATGCGCCACAAAGGAGCTAAACACCTTCGG 1445

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95211

seq_documentation_block:
ID   AAZ95211 standard; DNA; 978 BP.
XX
AC   AAZ95211;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B15 exon 5 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
KW   drug interaction; detect; human; single nucleotide polymorphism;
KW   SNPs; ds.
XX
OS   Homo sapiens.
XX
```

```
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions -
XX
PS   Example 3; Page 62; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 5 of the human
CC   UDP-glucuronosyltransferase 2B15 (UGT2B15) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC   the glucuronic acid conjugation of a wide range of endogenous and
CC   exogenous substrates. The UGT2B gene subfamily encode steroid
CC   metabolizing isoforms in the liver. Alteration of the expression or
CC   function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC   can be used to detect altered UGT2B metabolism of a substrate in an
CC   individual. The nucleic acid molecules comprising a human UGT2B sequence
CC   polymorphism can be used in screening assays for genotyping individuals,
CC   also to predict their rate of metabolism of UGT2B substrate, potential
CC   drug-drug interactions and adverse side effects. The polymorphisms can be
CC   used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC   linkage related to phenotypic variation in activity or expression of
CC   UGT2B protein. The polymorphism containing nucleic acid molecules may
CC   also be used for generating genetically modified non-human animals and
CC   for obtaining site specific gene modification in cell lines.
XX
SQ   Sequence 978 BP; 321 A; 187 C; 162 G; 308 T; 0 other;


alignment_scores:
            Quality:   23.00              Length:     23
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95211   ..

 Align seg 1/1  to: AAZ95211  from: 1  to: 978

     453 LysProLeuAspArgAlaValPheTrpIleGluPheValMetArgHisLy 469
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     378 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAGTTTGTCATGCGCCACAA 427

     469 sGlyAlaLysHisLeuArg 475
         |||||||||||||||||||
     428 AGGAGCCAAGCACCTTCGA 446

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95206

seq_documentation_block:
ID   AAZ95206 standard; DNA; 1976 BP.
XX
AC   AAZ95206;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UDP-glucuronosyltransferase 2B15 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
```

KW drug interaction; detect; human; single nucleotide polymorphism;
KW SNPs; ds.
XX
OS Homo sapiens.
XX
PN WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16675.
XX
PR 28-JUL-1998; 98US-0094391.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX
DR WPI; 2000-195321/17.
DR P-PSDB; AAY78935.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions
XX
PS Disclosure; Page 56-59; 72pp; English.
XX
CC This sequence represents the human UDP-glucuronosyltransferase 2B15
CC (UGT2B15) gene. UDP-glucuronosyltransferase (UGTs) are a family of
CC enzymes that catalyse the glucuronic acid conjugation of a wide range of
CC endogenous and exogenous substrates. The UGT2B gene subfamily encode
CC steroid metabolizing isoforms in the liver. Alteration of the expression
CC or function of UGTs may effect drug metabolism. The invention relates to
CC non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC sequence polymorphisms (see AAZ95051-Z95110). Probes which detect the
CC UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism
CC of a substrate in an individual. The nucleic acid molecules comprising a
CC human UGT2B sequence polymorphism can be used in screening assays for
CC genotyping individuals, also to predict their rate of metabolism of
CC UGT2B substrate, potential drug-drug interactions and adverse side
CC effects. The polymorphisms can be used as single nucleotide polymorphisms
CC (SNPs) for detecting genetic linkage related to phenotypic variation in
CC activity or expression of UGT2B protein. The polymorphism containing
CC nucleic acid molecules may also be used for generating genetically
CC modified non-human animals and for obtaining site specific gene
CC modification in cell lines.
XX
SQ Sequence 1976 BP; 594 A; 368 C; 419 G; 595 T; 0 other;

```
alignment_scores:
            Quality:   23.00              Length:     23
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95206   ..

 Align seg 1/1  to: AAZ95206  from: 1  to: 1976

     453 LysProLeuAspArgAlaValPheTrpIleGluPheValMetArgHisLy 469
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1376 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAGTTTGTCATGCGCCACAA 1425

     469 sGlyAlaLysHisLeuArg 475
         |||||||||||||||||||
    1426 AGGAGCCAAGCACCTTCGA 1444

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95210

seq_documentation_block:
ID   AAZ95210 standard; DNA; 1602 BP.
XX
AC   AAZ95210;
```

XX
DT 05-JUN-2000 (first entry)
XX
DE Human UGT2B15 exon 4 nucleotide sequence.
XX
KW UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
KW drug interaction; detect; human; single nucleotide polymorphism;
KW SNPs; ds.
XX
OS Homo sapiens.
XX
PN WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16675.
XX
PR 28-JUL-1998; 98US-0094391.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX
DR WPI; 2000-195321/17.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions
XX
PS Example 3; Page 62; 72pp; English.
XX
CC This sequence represents the nucleotide sequence of exon 4 of the human
CC UDP-glucuronosyltransferase 2B15 (UGT2B15) gene.
CC UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC the glucuronic acid conjugation of a wide range of endogenous and
CC exogenous substrates. The UGT2B gene subfamily encode steroid
CC metabolizing isoforms in the liver. Alteration of the expression or
CC function of UGTs may effect drug metabolism. The invention relates to
CC non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC can be used to detect altered UGT2B metabolism of a substrate in an
CC individual. The nucleic acid molecules comprising a human UGT2B sequence
CC polymorphism can be used in screening assays for genotyping individuals,
CC also to predict their rate of metabolism of UGT2B substrate, potential
CC drug-drug interactions and adverse side effects. The polymorphisms can be
CC used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC linkage related to phenotypic variation in activity or expression of
CC UGT2B protein. The polymorphism containing nucleic acid molecules may
CC also be used for generating genetically modified non-human animals and
CC for obtaining site specific gene modification in cell lines.
XX
SQ Sequence 1602 BP; 488 A; 285 C; 241 G; 588 T; 0 other;

```
alignment_scores:
            Quality:   15.00              Length:     15
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95210   ..

 Align seg 1/1  to: AAZ95210  from: 1  to: 1602

     360 LeuLeuGlyHisProLysThrLysAlaPheIleThrHisGlyGly 374
         |||||||||||||||||||||||||||||||||||||||||||||||
    1288 CTTTTAGGTCATCCCAAAACCAAAGCTTTTATAACTCATGGTGGA 1332

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95197

seq_documentation_block:
ID   AAZ95197 standard; DNA; 689 BP.
XX
```

```
AC   AAZ95197;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B4 exon 5 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B4; UGT2B4; polymorphism; metabolism; SNPs;
KW   drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions  -
XX
PS   Disclosure; Page 33; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 5 of the human
CC   UDP-glucuronosyltransferase 2B4 (UGT2B4) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC   the glucuronic acid conjugation of a wide range of endogenous and
CC   exogenous substrates. The UGT2B gene subfamily encode steroid
CC   metabolizing isoforms in the liver. Alteration of the expression or
CC   function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC   can be used to detect altered UGT2B metabolism of a substrate in an
CC   individual. The nucleic acid molecules comprising a human UGT2B sequence
CC   polymorphism can be used in screening assays for genotyping individuals,
CC   also to predict their rate of metabolism of UGT2B substrate, potential
CC   drug-drug interactions and adverse side effects. The polymorphisms can be
CC   used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC   linkage related to phenotypic variation in activity or expression of
CC   UGT2B protein. The polymorphism containing nucleic acid molecules may
CC   also be used for generating genetically modified non-human animals and
CC   for obtaining site specific gene modification in cell lines.
XX
SQ   Sequence 689 BP; 237 A; 109 C; 106 G; 237 T; 0 other;


alignment_scores:
            Quality:   13.00              Length:     13
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95197   ..

 Align seg 1/1  to: AAZ95197  from: 1  to: 689

     399 AspAsnIleAlaHisMetLysAlaLysGlyAlaAlaVal 411
         |||||||||||||||||||||||||||||||||||||||
     233 GATAACATTGCACACATGAAGGCCAAGGGAGCAGCTGTT 271

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95209

seq_documentation_block:
ID   AAZ95209 standard; DNA; 480 BP.
XX
```

```
AC   AAZ95209;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B15 exon 3 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
KW   drug interaction; detect; human; single nucleotide polymorphism;
KW   SNPs; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions  -
XX
PS   Example 3; Page 61; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 3 of the human
CC   UDP-glucuronosyltransferase 2B15 (UGT2B15) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC   the glucuronic acid conjugation of a wide range of endogenous and
CC   exogenous substrates. The UGT2B gene subfamily encode steroid
CC   metabolizing isoforms in the liver. Alteration of the expression or
CC   function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC   can be used to detect altered UGT2B metabolism of a substrate in an
CC   individual. The nucleic acid molecules comprising a human UGT2B sequence
CC   polymorphism can be used in screening assays for genotyping individuals,
CC   also to predict their rate of metabolism of UGT2B substrate, potential
CC   drug-drug interactions and adverse side effects. The polymorphisms can be
CC   used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC   linkage related to phenotypic variation in activity or expression of
CC   UGT2B protein. The polymorphism containing nucleic acid molecules may
CC   also be used for generating genetically modified non-human animals and
CC   for obtaining site specific gene modification in cell lines.
XX
SQ   Sequence 480 BP; 154 A; 75 C; 101 G; 150 T; 0 other;


alignment_scores:
            Quality:   12.00              Length:     12
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95209   ..

 Align seg 1/1  to: AAZ95209  from: 1  to: 480

     322 IleAlaSerAlaLeuAlaGlnIleProGlnLysVal 333
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     142 ATTGCATCAGCCCTTGCCCAGATCCCACAAAAGGTT 177

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95194

seq_documentation_block:
ID   AAZ95194 standard; DNA; 746 BP.
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XX
AC   AAZ95194;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B4 exon 2 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B4; UGT2B4; polymorphism; metabolism; SNPs;
KW   drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions  -
XX
PS   Disclosure; Page 32; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 2 of the human
CC   UDP-glucuronosyltransferase 2B4 (UGT2B4) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC   the glucuronic acid conjugation of a wide range of endogenous and
CC   exogenous substrates. The UGT2B gene subfamily encode steroid
CC   metabolizing isoforms in the liver. Alteration of the expression or
CC   function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC   can be used to detect altered UGT2B metabolism of a substrate in an
CC   individual. The nucleic acid molecules comprising a human UGT2B sequence
CC   polymorphism can be used in screening assays for genotyping individuals,
CC   also to predict their rate of metabolism of UGT2B substrate, potential
CC   drug-drug interactions and adverse side effects. The polymorphisms can be
CC   used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC   linkage related to phenotypic variation in activity or expression of
CC   UGT2B protein. The polymorphism containing nucleic acid molecules may
CC   also be used for generating genetically modified non-human animals and
CC   for obtaining site specific gene modification in cell lines.
XX
SQ   Sequence 746 BP; 253 A; 133 C; 118 G; 242 T; 0 other;


alignment_scores:
           Quality:   12.00            Length:     12
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95194   ..

 Align seg 1/1  to: AAZ95194  from: 1  to: 746

     273 GluPheValGlyGlyLeuHisCysLysProAlaLys 284
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     297 GAGTTCGTTGGAGGACTCCACTGCAAACCTGCCAAA 332

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ95208

seq_documentation_block:
ID   AAZ95208 standard; DNA; 1020 BP.
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XX
AC   AAZ95208;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B15 exon 2 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
KW   drug interaction; detect; human; single nucleotide polymorphism;
KW   SNPs; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions  -
XX
PS   Example 3; Page 61; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 2 of the human
CC   UDP-glucuronosyltransferase 2B15 (UGT2B15) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC   the glucuronic acid conjugation of a wide range of endogenous and
CC   exogenous substrates. The UGT2B gene subfamily encode steroid
CC   metabolizing isoforms in the liver. Alteration of the expression or
CC   function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC   can be used to detect altered UGT2B metabolism of a substrate in an
CC   individual. The nucleic acid molecules comprising a human UGT2B sequence
CC   polymorphism can be used in screening assays for genotyping individuals,
CC   also to predict their rate of metabolism of UGT2B substrate, potential
CC   drug-drug interactions and adverse side effects. The polymorphisms can be
CC   used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC   linkage related to phenotypic variation in activity or expression of
CC   UGT2B protein. The polymorphism containing nucleic acid molecules may
CC   also be used for generating genetically modified non-human animals and
CC   for obtaining site specific gene modification in cell lines.
XX
SQ   Sequence 1020 BP; 337 A; 156 C; 189 G; 338 T; 0 other;


alignment_scores:
           Quality:   12.00            Length:     12
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-784-340-2 x AAZ95208   ..

 Align seg 1/1  to: AAZ95208  from: 1  to: 1020

     254 TrpLeuIleArgThrTyrTrpAspPheGluPhePro 265
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     457 TGGCTCATTCGAACCTATTGGGATTTTGAATTTCCT 492
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